Poliovirus eradication is one of the most challenging public health endeavors in modern times (www.polioeradication.org). Social, political, economic & scientific factors have made this goal elusive. When eradication goals were first established in 1988, there was little appreciation of viral RNA recombination, enterovirus species groups and their relevance to eradication. Now, it is clear that RNA recombination between live-attenuated vaccine strains of poliovirus and non-polio group C enteroviruses results in circulating vaccine-derived polioviruses (cVDPV) and corresponding outbreaks of paralytic disease, a significant obstacle to eradication. By understanding enterovirus species groups, it becomes clear that poliovirus capsid proteins can be eradicated; however, the remainder of poliovirus RNA genomes will survive indefinitely in other group C enteroviruses. To help address these obstacles to eradication, the Barton lab studies molecular features of 3Dpol involved in viral RNA replication and recombination. A dsRNA clamp of 3Dpol that holds RNA products of replication as they exit the polymerase plays important roles in the polyadenylation of viral RNA, the fidelity of RNA replication, ribavirin sensitivity and viral RNA recombination. In other experiments, we identified a group C enterovirus RNA involved in the inhibition of ribonuclease L, an antiviral endoribonuclease. The RNase L cRNA plays an important but largely unexplored roles in pathogenesis. Using novel deep sequencing methods, we found that RNase L targets viral RNA encoding neutralizing epitopes of capsid proteins, sparing most other regions of viral RNA. These data suggest an important interplay between neutralizing antibodies, neutralization escape mutations and antiviral endoribonucleases. A better understanding of viral RNA recombination, enterovirus species groups and antiviral endoribonucleases should help achieve and maintain poliovirus eradication.

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Transcriptome markers of viral persistence in naturally-infected Andes Hantavirus (Bunyaviridae) seropositive rice rats
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The long-tailed pygmy rice rat (Oligoryzomys longicaudatus) is the reservoir host of Andes (ANDV) and Oran hantaviruses (Bunyaviridae). To examine transcriptome features of persistently infected rice rats, spleens
Animation of VZV DNA

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Varicella zoster virus (VZV) is a ubiquitous neurotropic alphaherpesvirus that typically causes childhood varicella (chickenpox) on primary infection and zoster (shingles) after reactivation. During latency most of the ~70 virus genes are transcriptionally silent; however, analysis of latent VZV gene transcription in its natural setting requires analysis of human ganglia removed at autopsy. Recognizing the problems associated with such samples, we have observed that as the post-mortem time interval increases, so do the number of VZV genes transcribed. Based on our data and recent similar findings concerning reactivation of HSV-1, we propose an interesting testable model to describe epigenetic control of neurotropic alphaherpesvirus gene transcription during latency and early reactivation.

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Viralign: A tool for uncovering functional viral elements

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The availability of broad epigenomic profiles of human tissues provides an opportunity to uncover viral sequences and their corresponding functional regulatory elements in otherwise overlooked datasets. We developed Viralign, a throughput screening method to discover and interpret viral functional information in existing short read archive data. Using a comprehensive reference database, Viralign scans sequence data for known viral sequences and generates an alignment report with read information and genome coverage. Viralign analyzes functional datasets for regulatory elements and provides coordinate and visualization files that can be viewed in a genome browser. Additionally, this method searches for potential integration sites and variants by genome assembly. In a pilot study, we performed H3K27me3 ChIP-seq in monocytes of an HHV6 infected individual and compared this to U2OS cells infected with HHV6A and HHV6B and use Viralign to detect HHV6 insertion loci and H3K27me3 enriched regions. The source code as well as additional data for Viralign will be made publicly available.

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Autophagic flux without a block differentiates varicella from herpes simplex virus infection

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Varicella-zoster virus (VZV) is a herpesvirus that causes a characteristic vesicular exanthem in humans with primary infection (varicella) or reactivation (zoster). We have previously observed that vesicular cells are filled with autophagosomes that are easily detectable by confocal microscopy after immunolabeling for the LC3 protein. Through a 3D imaging software program called Imaris we have quantitated autophagosomes as greater than 100 per cell. Similarly, we have assessed autophagy in VZV-infected monolayers after inoculation by the traditional method with infected cells at a ratio of one infected to 8 uninfected cells. Again, autophagosomes are easily detected, but their count is lower than that observed in human skin cells. As an additional control, we enumerated the autophagosomes in the Severe Combined Immuno-Deficient (SCID) Mouse model of VZV infection. In this model, human skin is inserted under the skin of the mouse and subsequently inoculated with VZV-infected cells. Again, autophagy was abundant in the VZV-infected skin and minimal in the mock-infected skin sample. Subsequently, we investigated autophagy following infection with sonically prepared cell free virus in cultured cells. After cell free virus inoculation, autophagy was detected in a majority of infected cells at all time points, but was less than that seen after an infected-cell inoculum. Finally, we investigated VZV-induced autophagic flux by two different methods (radiolabeling proteins and a dual-colored LC3 plasmid); both showed no evidence of a block in autophagy. Overall, therefore, autophagy within a VZV-infected cell was remarkably different from autophagy within an HSV-infected cell, whose genome contains two modifiers of autophagy, ICP34.5 and US11, not present in VZV.

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Recombination, reassortment, and many-to-one genotypes in natural arenavirus infections

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Mutation, recombination, and reassortment generate virus particles with variable genotypes, some of which may be better adapted to infect a new host, resist drug treatment, or escape immune pressure. The arenaviruses are a family of viruses that package a large (L) and small (S) genome segment. Arenaviruses infect mammals and snakes and are associated with fatal disease in both groups of animals. Although recombination and reassortment are well documented in some virus families, neither process has been observed in natural arenavirus infections. In this study, we documented a surprising degree of genetic diversity in arenavirus-infected snakes. Instead of one or two viral species or quasispecies, individual animals harbored complex populations of viral genotypes composed of up to 5 S and 11 L genotypes, which replicated as stable ensembles in culture. S and L segment genotype accumulation was not balanced and a particular S segment genotype dominated, both in individual animals and at a population level. Numerous instances of recombination and